



Sequence Viewer
Nucleotide

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Search		Nucleotide	for					Go	Clear
Limits		Preview/Index		History		Clipboard		Details	
Display	default	Save	Text	Add to Clipboard		Get Subsequence			

☐ 1: BC008489. Homo sapiens, hyp...[gi:14250143]MapView, Related Sequences, Protein, Taxonomy,
LinkOut

LOCUS BC008489 1798 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, hypothetical protein NUF2R, clone MGC:14815
IMAGE:4134468, mRNA, complete cds.
ACCESSION BC008489
VERSION BC008489.1 GI:14250143
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1798)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 21 Row: 1 Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction.

FEATURES
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BASE COUNT 673 a 290 c 352 g 483 t
ORIGIN

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Revised: July 5, 2002.

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